# A M E N D M E N T S

Please amend the subject application as set forth below.

<u>In the Claims</u>

Cancel claims 48 through 50 inclusive and 55 without prejudice.

Amend claims 51, 52, 56, 58, 60, and 62 through 68 inclusive as set forth below:

N.E.    Claims 51, 56, 62, 64, and 67, line 1, for "49" substitute - - 72 - -.

N.E.    Claims 52, 58, 63, 65, and 68, line 1, for "50" substitute - -74 - -.

N.E    Claims 60 and 66, line 1, for "48" substitute - - 72 - -.

Add the following new claims 72 through 74 inclusive.

--72.    (New) A method of determining both genotype and confidence scores at a genetic locus for a plurality of samples of genetic material wherein the plurality of samples have been prepared under comparable conditions, the method comprising:

(a)    assembling reaction-value data points for the samples, each reaction-value data point corresponding to a respective one of the samples and including at least one reaction value;

(b)    determining an initial conditional probability for each reaction-value data point for each genotype;

(c)    computing a conditional probability of each genotype for each reaction-value data point; and

(d)    determining the genotype and confidence score for each reaction-value data point, thus determining the genotype and confidence score at the genetic locus for each sample.

73.     (New) A method according to claim 72 wherein each reaction-value data point includes a first reaction value and a second reaction value.

74.     (New) A method according to claim 73 wherein the first reaction value is indicative of the presence of a first allele at the locus and the second reaction value is indicative of the presence of a second allele at the locus.--

## R E M A R K S

A.      Summary of the Invention

Broadly, the subject invention concerns a method for determining both genotype and confidence scores at a genetic locus for a plurality of samples of genetic material prepared under comparable conditions. The method of the invention includes a step of assembling reaction-data points for the samples. Each reaction-value data point corresponds to one of the samples and includes at least one reaction value. The method of the invention includes the step of determining an initial probability for each reaction-value data point for each genotype and computing a conditional probability of each genotype for each reaction-value data point. The genotype and confidence score is determined for each reaction-value data point to determine the genotype and confidence score at the genetic locus for each sample.